Please amend the application as follows:

In the Specification:

At page 11, please replace the paragraph beginning at line 6 with the following paragraph:

As used herein the term "autologous" with reference to a polypeptide of the invention includes self polypeptides and variants thereof (or the nucleic acid molecules that encode them) that are sufficiently homologous to (i.e., share sufficient nucleotide or amino acid sequence identity with) an autologous target polypeptide (or nucleic acid molecule encoding it) that they can promote an immune response to the target autologous antigen. Preferably, an autologous polypeptide is derived from the same species as the subject to which a composition comprising that polypeptide is administered. In one embodiment, autologous polypeptides can be replaced with polypeptides from another species that are sufficiently homologous to an autologous polypeptide. For example, if a polypeptide from a human and a polypeptide from a mouse contain highly conserved stretches of amino acids, peptides derived from the highly conserved mouse polypeptide may be functionally equivalent to the human polypeptide, in that the mouse polypeptide can promote the development of an anti-human target antigen immune response. In this example, because the polypeptide from the mouse is sufficiently homologous to the human polypeptide to promote an immune response to the human target autologous antigen in the subject, the mouse polypeptide ~~is can be used~~ can be used in the subject constructs in place of an "autologous." Polypeptides are said to be functionally equivalent to an autologous polypeptide if they are sufficiently homologous to an autologous polypeptide to promote an anti-target antigen immune response in a subject.

At page 19, please replace the paragraph beginning at line 16 with the following paragraph:

The nucleic acid and protein sequences of the CTLA4 can further be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, et al. (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to CTLA4 nucleic acid molecules of the invention.

BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a reference polypeptide of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. ~~See http//www.ncbi.nlm.nih.gov~~. See the NCBI web site

At page 53, please replace the paragraph beginning at line 17 with the following paragraph:

15 Balb/c mice were immunized with mIgβ-hIgG.Fc proteins independently, once per two weeks. One week after every boost, about ~~100 ml~~ 100 µl of blood was collected from each immunized mouse for the quantification of B-/T-lymphocyte ratio changes. The anti-sera were also prepared for the identification of titer specificity.